



SEQUENCE LISTING

<110> Young, Karen K. Y.
Roche Molecular Systems, Inc.

<120> Compositions and Methods for Detecting Certain
Flaviviruses, Including Members of the Japanese
Encephalitis Virus Serogroup

<130> 022101-000230US

<140> US 10/815,480

<141> 2004-03-31

<150> US 60/459,491

<151> 2003-03-31

<150> US 60/552,454

<151> 2004-03-12

<150> US 60/555,530

<151> 2004-03-22

<160> 74

<170> PatentIn Ver. 2.1

<210> 1

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conserved sequence in 3' untranslated region of
the genomes of flaviviruses

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<220>

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25

<210> 3

<211> 26

<212> DNA

<213> Artificial Sequence

<220>
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 encephalitis virus serogroup Primer 1

 <220>
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 <223> n = t or absent

 <400> 3
 gwaascnsy crramcysy tcggrw 26

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 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:West Nile virus
 Primer 1

 <220>
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 <222> (8)
 <223> n = t or absent

 <400> 4
 gtaagccncy cagaaccgyy tcggaa 26

 <210> 5
 <211> 26
 <212> DNA
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 <220>
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 encephalitis virus Primer 1

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 <222> (8)
 <223> n = absent

 <400> 5
 gaaascnct crraacygty tcggaa 26

 <210> 6
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:Murray Valley
 encephalitis virus Primer 1

 <400> 6
 gaaagcctcc cagamccgty tcggaa 26

<210> 7
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 <212> DNA
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 <223> Description of Artificial Sequence:Koutango virus
 Primer 1

 <400> 7
 gtaagccctc agaaccgtct cggaa 25

 <210> 8
 <211> 25
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 <220>
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 gtaagccctc agaaccgtct cggaa 25

 <210> 9
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:region of
 conserved sequence in 3' untranslated region of
 the genomes of flaviviruses

 <400> 9
 tctcctagtc tatcccaggt gtcaa 25

 <210> 10
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 <213> Artificial Sequence

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 SEQ ID NO:9

 <400> 10
 agaggatcag atagggtcca cagtt 25

 <210> 11
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:Japanese
 encephalitis virus serogroup Primer 2

<220>
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 <222> (11)
 <223> n = t or absent

 <400> 11
 yccyastmtw nyyccaggtr tcaa 24

 <210> 12
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
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 Primer 2

 <400> 12
 ycctagtcta tcccaggtrt caa 23

 <210> 13
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
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 encephalitis virus Primer 2

 <400> 13
 cccyastmta tyyccagggtg tcaa 24

 <210> 14
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
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 encephalitis virus Primer 2

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 tcctagtctt ttcccagggtg tcaa 24

 <210> 15
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
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 2

 <400> 15
 tcctagtcta tcccagggtg caa 23

<210> 16
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:region of conserved sequence in 3' untranslated region of the genomes of flaviviruses

 <400> 16
 ggactagagg ttagaggaga ccccgcgg 28

 <210> 17
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:complement of SEQ ID NO:16

 <400> 17
 ccgcgggggc tcctctaacc tctagtcc 28

 <210> 18
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:probe for detecting flaviviruses

 <220>
 <221> modified_base
 <222> (25)
 <223> n = g, c, t, a or absent

 <220>
 <221> modified_base
 <222> (26)
 <223> n = c, t, g or absent

 <220>
 <221> modified_base
 <222> (27)
 <223> n = g, c, a, t or absent

 <220>
 <221> modified_base
 <222> (28)
 <223> n = g, c, a, t or absent

 <400> 18
 ggwctagwgg ttagaggaga ccynnnnn 28

<210> 19
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:probe for
 detecting Japanese encephalitis virus serogroup
 members

 <400> 19
 ggactagwgg ttagaggaga ccccrykk 28

 <210> 20
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:probe for
 detecting West Nile virus

 <400> 20
 ggactagwgg ttagaggaga cccrcgk 28

 <210> 21
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:probe for
 detecting Japanese encephalitis virus

 <400> 21
 ggactagagg ttagaggaga ccccgygg 28

 <210> 22
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:probe for
 detecting Murray Valley encephalitis virus

 <400> 22
 ggactagagg ttagaggaga cccactc 28

 <210> 23
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:probe for
 detecting Kunjin virus

<400> 23
 aataygtgga ttacatgast tcaytgaag 29

<210> 24
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:probe for
 detecting Dengue virus

<400> 24
 ggactagagg ttagaggaga ccccyssv 28

<210> 25
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:probe for
 detecting yellow fever virus

<400> 25
 ggtctagagg ttagaggaga ccctccag 28

<210> 26
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:probe for
 detecting Montana myotis leukencephalitis virus

<400> 26
 ggactagagg ttagaggaga ccccttcc 28

<210> 27
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:probe for
 detecting Modoc virus

<400> 27
 ggactagagg ttgagggaga cccccggc 28

<210> 28
 <211> 28
 <212> DNA
 <213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence:Example Probe 1

<400> 28
ggactagagg ttagaggaga ccccgcgg                                28

<210> 29
<211> 418
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:3' untranlated
      region of the genome of St. Louis encephalitis
      virus (SLEV) isolate BFS1750

<400> 29
ttgccaccgg atgtcaggta aacggtgctg tctgtaacct ggccccaggt gactgggtta 60
tcaaagccaa tctggccgag tgcaaagccc ctcatgccga ctcgaggagg tccctagcac 120
gtaggctgga gaggacgcaa aagtcagacc agaaatgcc cctgaaagca tgctaaaggt 180
gctgtctgta catgccccag gaggactggg ttaacaaagc ttaacagccc cagcggccca 240
aaccatggag tgcgtgacca tggcgtaagg actagaggtt agaggagacc ccgctgcaac 300
ttggcaaggc ccaaaccgcg tcgaagctgt agagacgggg gaaggactag aggttagagg 360
agacccttgc ccgttaacgc aaacaacagc atattgacac ctggaaagac aggagatc 418

<210> 30
<211> 342
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:3' untranlated
      region of the genome of St. Louis encephalitis
      virus (SLEV) isolate 1750-Std

<400> 30
ttgccaccgg atgtcaggta aacggtgctg tctgtaacct ggccccaggt gactgggtta 60
tcaaagccaa tctggccgag tgcaaagccc ctcatgccga ctcgaggagg tccctagcac 120
gtaggctgga gaggacgcaa aagtcagacc agaaatgcc cctgaaagca tgctaaaggt 180
gctgtctgta catgccccag gaggactggg ttaacaaagc ttaacagccc cagcggccca 240
aaccatggag tgcgtgacca tggcgtaagg actagaggtt agaggagacc ccgcgcaact 300
tggcaaggcc caaaccgcgt cgaagctgta gagacggggg aa                      342

<210> 31
<211> 418
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:3' untranlated
      region of the genome of St. Louis encephalitis
      virus (SLEV) isolate TD6-4G

<400> 31
ttgccaccgg atgtcaggta aacggtgctg cctgtaacct ggccccaggt gactgggtta 60
tcaaagccaa tctggccgag tgcaaagccc ctcatgccga ctcgaggagg tccctggcac 120
gtaggctgga gaggacgcaa aagtcagacc agaaatgcc cctgaaagca tgctaaaggt 180
gctgtctgta catgccccag gaggactggg ttaacaaagc ttaacagccc cagcggccca 240

```

aaccatggag tgcgtgacca tggcgtaagg actagaggtt agaggagacc ccgctgcaac 300
 tcggcaaggc ccaaaccgc tcgaagctgt agagatgggg gaaggactag aggttagagg 360
 agacccttg ccgttaacgc aaacaacagc atattgacac ctggaaagac aggagatc 418

<210> 32
 <211> 342
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:3' untranlated
 region of the genome of St. Louis encephalitis
 virus (SLEV) isolate CoaV750

<400> 32
 ttgccaccgg atgtcaggta aacggtgctg cctgtaacct ggccccaggt gactgggtta 60
 ccaaagccaa tctggctgag tgcaaagccc ctcgttccga ttcgggaggg tccctggcac 120
 gtaggctgga gaggacgcaa aagtcagacc agaaatgcc cctgaaagca tgctaaaggt 180
 gctgtctgta catgccccag gaggactggg ttaacaaagc ttaacagccc cagcggccca 240
 aaccatggag tgcgtgacca tggcgtaagg actagaggtt agaggagacc ccgcgcaact 300
 tggcaaggcc aaaaccgcgt cgaagctgta gagatggggg aa 342

<210> 33
 <211> 418
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:3' untranlated
 region of the genome of St. Louis encephalitis
 virus (SLEV) isolate L695121.05

<400> 33
 ttgccaccgg atgtcaggta aacggtgctg tctgtaacct ggccccaggt gactgggtta 60
 tcaaagccaa tccggctggg tgcaaagccc ctcattccga ctcgggaggg tccctggcat 120
 gtaggctgga gaggacgcac aagtcagacc agaaatgcc cctgaaagca tgctaaaggt 180
 gctgtctgta catgccccag gaggactggg ttaacaaagc ttaacagccc cagcggccca 240
 aaccatggag tgcgtgacca tggcgtaagg actagaggtt agaggagacc ccgctgtaac 300
 ttggcaaggc ccaaaccgc tcgaagctgt agagacgggg gaaggactag aggttagagg 360
 agacccttg ccgttaacgc aaacaacagc atattgacac ctggaaagac aggagatc 418

<210> 34
 <211> 418
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:3' untranlated
 region of the genome of St. Louis encephalitis
 virus (SLEV) isolate TNM771K

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 <221> modified_base
 <222> (384)
 <223> n = g, a, c or t

<400> 34
 ttgccaccgg atgtcaggta aacggtgctg tctgtaacct ggccccaggt gactgggtca 60

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tcaaagccaa tctggctggg tgcaaagccc ctcattccga ctcgggaggg tccctggcac 120
gtaggctgga gaggacgcac aagtcagacc agaaatgcc a cctgaaagca tgctaaaggt 180
gctgtctgta catgccccag gaggactggg ttaacaaagc ttaacagccc cagcggccca 240
aaccatggag agcgtgacca tggcgtaagg actagagggt agaggagacc ccgctgtaac 300
ttggcaaggc ccaaaccgc tcgaagctgt agagacgggg gaaggactag aggttagagg 360
agacccttg ccgttaacgc aaanaacagc atattgacac ctggaaagac aggagatc 418
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<210> 35

<211> 418

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:3' untranlated
region of the genome of St. Louis encephalitis
virus (SLEV) isolate MSI-7

<400> 35

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ttgccaccgg atgtcaggta aacggtgctg tctgtaacct ggccccaggc gactggggtta 60
tcaaagccaa tccggctggg tgcaaagccc ctcattccga ctcgggaggg tccctggcac 120
gtaggctgga gaggacgcac aagtcagacc agaaatgcc a cctgaaagca tgctaaaggt 180
gctgtctgta catgccccag gaggactggg ttaacaaagc ttaacagccc cagcggccca 240
aaccatggag tgcgtgacca tggcgtaagg actagagggt agaggagacc ccgctgtaac 300
ttggcaaggc ccaaaccgc tcaaagctgt agagacgggg gaaggactag aggttagagg 360
agacccttg ccgttaacgc aaacaacagc atattgacac ctggaaagac aggagatc 418
```

<210> 36

<211> 405

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:3' untranlated
region of the genome of St. Louis encephalitis
virus (SLEV) isolate Kern217

<400> 36

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ccgatgtca ggtaaacggt gctgtctgta acctggcccc aggtcactgg gttatcaaag 60
ccaaccggc tgggtgcaaa gccctcatt ccgactcggg agggtccttg gcacgtaggc 120
tggagaggac gcacaagtca gaccagaaat gccacctgaa agcatgctaa aggtgctgtc 180
tgtacatgcc ccaggaggac tgggttaaca aagcttaaca gcccagcgg ccaaaccat 240
ggagtgcgtg accatggcgt aaggactaga ggtagagga gaccccgctg taacttggca 300
aggcccaaac ccgctcaaag ctgtagagac gggggaagga ctagagggtta gaggagacc 360
cttgccgtta acgcaaaaca cagcatattg acacctggaa agaca 405
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<210> 37

<211> 375

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:3' untranlated
region of the genome of St. Louis encephalitis
virus (SLEV) isolate CoaV608

<400> 37

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cccaggcgac tgggttatca aagccaatcc ggctgggtgc aaagcccctc attccgactc 60
gggaggggtcc ctggcacgta ggctggagag gacgcacaag tcagaccaga aatgccacct 120
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```

gaaagcatgc taaaggtgct gtctgtacat gccccaggag gactgggtta acaaagctta 180
acagccccag cggcccaaac catggagtgc gtgaccatgg cgtaaggact agagggttaga 240
ggagaccccg ctgtaacttg gcaaggccca aaccgctca aagctgtaga gacgggggaa 300
ggactagagg ttagaggaga ccccttgccg ttaacgcaa caacagcata ttgacacctg 360
gaaagacagg agatc 375

```

```

<210> 38
<211> 411
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence:3' untranlated
      region of the genome of St. Louis encephalitis
      virus (SLEV) isolate TBH-28

```

```

<400> 38
ttgccaccgg atgtcaggta aacggtgctg tctgtaacct ggccccagggt gactgggtta 60
tcaaagccaa cccggctggg tgcaaagccc ctcatccga ctggggaggg tccctggcac 120
gtaggccgga gaggacgcac aagtcagacc agaaatgcca cctgaaagca tgctaaaggt 180
gctgtctgta catgccccag gaggactggg ttaacaaagc ttaacagccc cagcggccca 240
aaccatggag tgcgtgacca tggcgtaagg actagagggt agaggagacc ccgctgtaat 300
ttggcaaggc ccaaaccgc tcgaagctgt agagacgggg gaaggactag aggttagagg 360
agacccttg ccgttaacgc aaacaacagc atattgacac ctggaaagac a 411

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```

<210> 39
<211> 402
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence:3' untranlated
      region of the genome of St. Louis encephalitis
      virus (SLEV) isolate VR1265

```

```

<400> 39
ccggaagtca ggtaaacggt gctgtctgta acctggcccc aggtgactgg gttatcaaag 60
ccaatctggc tgggtgcaaa gccctcatt ccgactcggg agggtccttg gcacgtaggc 120
tggagcggac gcacaagtca gaccagaaat gccacctgaa agcatgctaa aggtgctgtc 180
tgtacatgcc ccaggaggac tgggttaaca aagcttaaca gccccagcgg cccaaaccat 240
ggagtgcgtg accatggcgt aaggactaga ggtagagga gaccccgctg taacttggca 300
aggcccaaac ccgctcgaag ctgtagagac gggggaagga ctagaggta gaggagacc 360
cttgccgtca acgcaaacaa cagcatattg acacctggaa ag 402

```

```

<210> 40
<211> 374
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence:3' untranlated
      region of the genome of St. Louis encephalitis
      virus (SLEV) isolate CoaV353

```

```

<400> 40
cccagggtgac tgggttatca aagccaatct agctgagtgc aaagcccctc attccgactc 60
gggaggggtcc ctggcacgta ggctggagag gacgcaaaag tcagaccaga aatgccacct 120
gaaagcatgc taaaggtgct gtctgtacat gccccaggag gactgggtta acaaagctta 180

```

```

acagccccag cggcccaaac catggagtgc gtgaccatgg cgtaaggact agaggttaga 240
ggagaccccc ctgcaacttg gcaaggccca aaccgctcg aagctgtaga gacgggggaa 300
ggactagagg ttagaggaga ccccttgccg ttaacgcaa caacagcata ttgacacctg 360
gaaagacagg agat 374

```

```

<210> 41
<211> 27
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence:Dengue virus
consensus upstream primer

```

```

<400> 41
gagccccgtc caaggacgta aaaagaa 27

```

```

<210> 42
<211> 27
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence:Dengue virus
consensus upstream primer

```

```

<220>
<221> modified_base
<222> (27)
<223> n = t-butyl-benzyl-dA

```

```

<400> 42
gagccccgtc caaggacgta aaaagan 27

```

```

<210> 43
<211> 27
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence:Dengue virus
consensus upstream primer

```

```

<220>
<221> modified_base
<222> (26)
<223> n = methyl-dA

```

```

<220>
<221> modified_base
<222> (27)
<223> n = t-butyl-benzyl-dA

```

```

<400> 43
gagccccgtc caaggacgta aaaagnn 27

```

<210> 44
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:Dengue virus
 type I upstream primer

 <400> 44
 gagccccgta caaggacgta aaatgaa 27

 <210> 45
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:Dengue virus
 type I upstream primer

 <220>
 <221> modified_base
 <222> (27)
 <223> n = t-butyl-benzyl-dA

 <400> 45
 gagccccgta caaggacgta aaatgan 27

 <210> 46
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:Dengue virus
 type I upstream primer

 <220>
 <221> modified_base
 <222> (26)
 <223> n = methyl-dA

 <220>
 <221> modified_base
 <222> (27)
 <223> n = t-butyl-benzyl-dA

 <400> 46
 gagccccgta caaggacgta aaatgnn 27

 <210> 47
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:Dengue virus
 types II and III upstream primer

 <400> 47
 gagccccgtc caaggacgtt aaaagaa 27

 <210> 48
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:Dengue virus
 types II and III upstream primer

 <220>
 <221> modified_base
 <222> (27)
 <223> n = t-butyl-benzyl-dA

 <400> 48
 gagccccgtc caaggacgtt aaaagan 27

 <210> 49
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:Dengue virus
 types II and III upstream primer

 <220>
 <221> modified_base
 <222> (26)
 <223> n = methyl-dA

 <220>
 <221> modified_base
 <222> (27)
 <223> n = t-butyl-benzyl-dA

 <400> 49
 gagccccgtc caaggacgtt aaaagnn 27

 <210> 50
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:Dengue virus
 type IV upstream primer

 <400> 50
 attgaagtca ggccacttgt gcca 24

<210> 51
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:Dengue virus
 type IV upstream primer

 <220>
 <221> modified_base
 <222> (24)
 <223> n = t-butyl-benzyl-dA

 <400> 51
 attgaagtca ggccacttgt gccn 24

 <210> 52
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:Dengue virus
 type IV upstream primer

 <220>
 <221> modified_base
 <222> (23)
 <223> n = ethyl-dC

 <220>
 <221> modified_base
 <222> (24)
 <223> n = t-butyl-benzyl-dA

 <400> 52
 attgaagtca ggccacttgt gcnn 24

 <210> 53
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:Dengue virus
 downstream primer

 <400> 53
 gatctctgggt ctttcccagc gtcaa 25

 <210> 54
 <211> 25
 <212> DNA
 <213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence:Dengue virus
        downstream primer

<220>
<221> modified_base
<222> (25)
<223> n = t-butyl-benzyl-dA

<400> 54
gatctctggt ctttcccagc gtcan
25

<210> 55
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Dengue virus
        downstream primer

<220>
<221> modified_base
<222> (24)
<223> n = methyl-dA

<220>
<221> modified_base
<222> (25)
<223> n = t-butyl-benzyl-dA

<400> 55
gatctctggt ctttcccagc gtcnn
25

<210> 56
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:yellow fever
        virus upstream primer

<400> 56
aaccgggata aaaactacgg gtggagaa
28

<210> 57
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:yellow fever
        virus upstream primer

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<220>
 <221> modified_base
 <222> (28)
 <223> n = t-butyl-benzyl-dA

 <400> 57
 aaccgggata aaaactacgg gtggagan 28

 <210> 58
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:yellow fever
 virus upstream primer

 <220>
 <221> modified_base
 <222> (27)
 <223> n = methyl-dA

 <220>
 <221> modified_base
 <222> (28)
 <223> n = t-butyl-benzyl-dA

 <400> 58
 aaccgggata aaaactacgg gtggagnn 28

 <210> 59
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:yellow fever
 virus upstream primer

 <400> 59
 ataaaaacta cgggtggaga accgga 26

 <210> 60
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:yellow fever
 virus upstream primer

 <220>
 <221> modified_base
 <222> (26)
 <223> n = t-butyl-benzyl-dA

 <400> 60
 ataaaaacta cgggtggaga accggn 26

<210> 61
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:yellow fever
virus downstream primer

<400> 61
actccggtct ttccctggcg tcaa

24

<210> 62
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:yellow fever
virus downstream primer

<220>
<221> modified_base
<222> (24)
<223> n = t-butyl-benzyl-dA

<400> 62
actccggtct ttccctggcg tcan

24

<210> 63
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:yellow fever
virus downstream primer

<220>
<221> modified_base
<222> (23)
<223> n = methyl-dA

<220>
<221> modified_base
<222> (24)
<223> n = t-butyl-benzyl-dA

<400> 63
actccggtct ttccctggcg tcnn

24

<210> 64
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:St Louis
 encephalitis virus upstream primer

<400> 64
 caaagcccct cattccgact cggga 25

<210> 65
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:St Louis
 encephalitis virus upstream primer

<220>
 <221> modified_base
 <222> (25)
 <223> n = t-butyl-benzyl-dA

<400> 65
 caaagcccct cattccgact cgggn 25

<210> 66
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:St Louis
 encephalitis virus upstream primer

<400> 66
 tctcctgtct ttccaggtgt caa 23

<210> 67
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:St Louis
 encephalitis virus upstream primer

<220>
 <221> modified_base
 <222> (23)
 <223> n = t-butyl-benzyl-dA

<400> 67
 tctcctgtct ttccaggtgt can 23

<210> 68
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:St.Louis
 encephalitis virus (SLEV) first primer complement

 <400> 68
 ttgacacctg gaaagacagg aga 23

 <210> 69
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:St.Louis
 encephalitis virus (SLEV) second primer

 <400> 69
 caaagcccct cattccgact cggg 24

 <210> 70
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:flavivirus
 anti-sense probe

 <400> 70
 ggggtctctc taacctctag tccttcccc 30

 <210> 71
 <211> 98
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:region of
 conserved sequence in 3' untranslated region of
 the genome of flavivirus AF196835

 <400> 71
 caaccccagg aggactgggt gaacaaagcc gccaagtgat ccatgtaagc cctcagaacc 60
 gtctcggaag gaggaccca catgttgtaa cttcaaag 98

 <210> 72
 <211> 105
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:region of
 conserved sequence in 3' untranslated region of
 the genome of flavivirus AF196835

<400> 72
tgactgaagc ttaggtcag ggaaggact agaggtagt ggagaccccg tgccacaaaa 60
caccacaaca aaacagcata ttgacacctg ggatagacta ggaga 105

<210> 73
<211> 121
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:region of
conserved sequence in 3' untranslated region of
the genome of flavivirus AF196835

<400> 73
cagggcgaaa ggactagagg ttagaggaga cccgcgggtt taaagtgcac ggcccagcct 60
gactgaagct gtaggtcagg ggaaggacta gaggttagtg gagaccccggt gccacaaaac 120
a 121

<210> 74
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Example Primer 2

<400> 74
tctcctagtc tatcccaggt gtcaa 25